

EP 1 131 447 B1

Glu Gly Tyr Gln Ser Ser Gly Thr Ser Ser Ile Asn Val Gly Gly
 180 185 190

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<210> 11

<211> 191

<212> PRT

<213> Streptomyces lividans

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<400> 11

Ala Thr Thr Ile Thr Thr Asn Gln Thr Gly Thr Asp Gly Met Tyr Tyr
 1 5 10 15

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Ser Phe Trp Thr Asp Gly Gly Gly Ser Val Ser Met Thr Leu Asn Gly
 20 25 30

Gly Gly Ser Tyr Ser Thr Gln Trp Thr Asn Cys Gly Asn Phe Val Ala
 35 40 45

20

Gly Lys Gly Trp Ser Thr Gly Asp Gly Asn Val Arg Tyr Asn Gly Tyr
 50 55 60

25

Phe Asn Pro Val Gly Asn Gly Tyr Gly Cys Leu Tyr Gly Trp Thr Ser
 65 70 75 80

Asn Pro Leu Val Glu Tyr Tyr Ile Val Asp Asn Trp Gly Ser Tyr Arg
 85 90 95

30

Pro Thr Gly Thr Tyr Lys Gly Thr Val Ser Ser Asp Gly Gly Thr Tyr
 100 105 110

Asp Ile Tyr Gln Thr Thr Arg Tyr Asn Ala Pro Ser Val Glu Gly Thr
 115 120 125

35

Lys Thr Phe Gln Gln Tyr Trp Ser Val Arg Gln Ser Lys Val Thr Ser
 130 135 140

Gly Ser Gly Thr Ile Thr Thr Gly Asn His Phe Asp Ala Trp Ala Arg
 145 150 155 160

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Ala Gly Met Asn Met Gly Gln Phe Arg Tyr Tyr Met Ile Asn Ala Thr
 165 170 175

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Glu Gly Tyr Gln Ser Ser Gly Ser Ser Asn Ile Thr Val Ser Gly
 180 185 190

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<210> 12

<211> 189

<212> PRT

<213> Streptomyces sp.

<400> 12

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EP 1 131 447 B1

Ala Thr Thr Ile Thr Asn Glu Thr Gly Tyr Asp Gly Met Tyr Tyr Ser
 1 5 10 15
 Phe Trp Thr Asp Gly Gly Gly Ser Val Ser Met Thr Leu Asn Gly Gly
 20 25 30
 Gly Ser Tyr Ser Thr Arg Trp Thr Asn Cys Gly Asn Phe Val Ala Gly
 35 40 45
 Lys Gly Trp Ala Asn Gly Gly Arg Arg Thr Val Arg Tyr Thr Gly Trp
 50 55 60
 Phe Asn Pro Ser Gly Asn Gly Tyr Gly Cys Leu Tyr Gly Trp Thr Ser
 65 70 75 80
 Asn Pro Leu Val Glu Tyr Tyr Ile Val Asp Asn Trp Gly Ser Tyr Arg
 85 90 95
 Pro Thr Gly Glu Thr Arg Gly Thr Val His Ser Asp Gly Gly Thr Tyr
 100 105 110
 Asp Ile Tyr Lys Thr Thr Arg Tyr Asn Ala Pro Ser Val Glu Ala Pro
 115 120 125
 Ala Ala Phe Asp Gln Tyr Trp Ser Val Arg Gln Ser Lys Val Thr Ser
 130 135 140
 Gly Thr Ile Thr Thr Gly Asn His Phe Asp Ala Trp Ala Arg Ala Gly
 145 150 155 160
 Met Asn Met Gly Asn Phe Arg Tyr Tyr Met Ile Asn Ala Thr Glu Gly
 165 170 175
 Tyr Gln Ser Ser Gly Ser Ser Thr Ile Thr Val Ser Gly
 180 185

<210> 13

<211> 189

<212> PRT

<213> Thermomonospora fusca

<400> 13

Ala Val Thr Ser Asn Glu Thr Gly Tyr His Asp Gly Tyr Phe Tyr Ser
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 Phe Trp Thr Asp Ala Pro Gly Thr Val Ser Met Glu Leu Gly Pro Gly
 20 25 30
 Gly Asn Tyr Ser Thr Ser Trp Arg Asn Thr Gly Asn Phe Val Ala Gly
 35 40 45

EP 1 131 447 B1

Lys Gly Trp Ala Thr Gly Gly Arg Arg Thr Val Thr Tyr Ser Ala Ser
50 55 60

5 Phe Asn Pro Ser Gly Asn Ala Tyr Leu Thr Leu Tyr Gly Trp Thr Arg
65 70 75 80

Asn Pro Leu Val Glu Tyr Tyr Ile Val Glu Ser Trp Gly Thr Tyr Arg
85 90 95

10 Pro Thr Gly Thr Tyr Met Gly Thr Val Thr Thr Asp Gly Gly Thr Tyr
100 105 110

15 Asp Ile Tyr Lys Thr Thr Arg Tyr Asn Ala Pro Ser Ile Glu Gly Thr
115 120 125

Arg Thr Phe Asp Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg Thr Ser
130 135 140

20 Gly Thr Ile Thr Ala Gly Asn His Phe Asp Ala Trp Ala Arg His Gly
145 150 155 160

Met His Leu Gly Thr His Asp Tyr Met Ile Met Ala Thr Glu Gly Tyr
165 170 175

25 Gln Ser Ser Gly Ser Ser Asn Val Thr Leu Gly Thr Ser
180 185

30 <210> 14
<211> 190
<212> PRT
<213> Trichoderma harzianum
<400> 14

35 Gln Thr Ile Gly Pro Gly Thr Gly Tyr Ser Asn Gly Tyr Tyr Tyr Ser
1 5 10 15

40 Tyr Trp Asn Asp Gly His Ala Gly Val Thr Tyr Thr Asn Gly Gly Gly
20 25 30

Gly Ser Phe Thr Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
35 40 45

45 Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
50 55 60

Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Ile Tyr Gly Trp Ser
65 70 75 80

50 Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
85 90 95

55

EP 1 131 447 B1

5 Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
100 105 110
Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
115 120 125
10 Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
130 135 140
Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145 150 155 160
15 Ser His Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
165 170 175
Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185 190
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<210> 15

<211> 178

<212> PRT

<213> Trichoderma reesei

<400> 15

30 Ala Ser Ile Asn Tyr Asp Gln Asn Tyr Gln Thr Gly Gly Gln Val Ser
1 5 10 15
Tyr Ser Pro Ser Asn Thr Gly Phe Ser Val Asn Trp Asn Thr Gln Asp
20 25 30
35 Asp Phe Val Val Gly Val Gly Trp Thr Thr Gly Ser Ser Ala Pro Ile
35 40 45
Asn Phe Gly Gly Ser Phe Ser Val Asn Ser Gly Thr Gly Leu Leu Ser
50 55 60
40 Val Tyr Gly Trp Ser Thr Asn Pro Leu Val Glu Tyr Tyr Ile Met Glu
65 70 75 80
45 Asp Asn His Asn Tyr Pro Ala Gln Gly Thr Val Lys Gly Thr Val Thr
85 90 95
Ser Asp Gly Ala Thr Tyr Thr Ile Trp Glu Asn Thr Arg Val Asn Glu
100 105 110
50 Pro Ser Ile Gln Gly Thr Ala Thr Phe Asn Gln Tyr Ile Ser Val Arg
115 120 125
Asn Ser Pro Arg Thr Ser Gly Thr Val Thr Val Gln Asn His Phe Asn
130 135 140
55

EP 1 131 447 B1

5 Trp Ala Ser Leu Gly Leu His Leu Gly Gln Met Met Asn Tyr Gln Val
 145 150 155 160
 Val Ala Val Glu Gly Trp Gly Gly Ser Gly Ser Ala Ser Gln Ser Val
 165 170 175
 10 Ser Asn
 <210> 18
 <211> 190
 <212> PRT
 15 <213> Trichoderma reesei
 <400> 18
 Gln Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
 1 5 10 15
 20 Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
 20 25 30
 25 Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
 35 40 45
 Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
 50 55 60
 30 Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
 65 70 75 80
 Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
 85 90 95
 35 Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
 100 105 110
 40 Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
 115 120 125
 Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
 130 135 140
 45 Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
 145 150 155 160
 Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
 165 170 175
 50 Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
 180 185 190
 55 <210> 17
 <211> 190
 <212> PRT

EP 1 131 447 B1

<213> Trichoderma viride
<400> 17

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5      Gln Thr Ile Gln Pro Gly Thr Gly Phe Asn Asn Gly Tyr Phe Tyr Ser
      1              5              10              15

      Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
              20              25              30

10     Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
              35              40              45

      Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
      50              55              60

15     Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
      65              70              75              80

      Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
      85              90              95

      Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
      100             105             110

25     Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
      115             120             125

      Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Thr His
      130             135             140

30     Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
      145             150             155             160

      Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
      165             170             175

35     Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
      180             185             190

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<210> 18

<211> 586

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence: TrX synthetic sequence

<400> 18

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55

EP 1 131 447 B1

ctagctaagg aggctgcaga tgcaaacaaat acaaccaggga accgggttaca acaacgggtta 60
 cttctacagc tattggaacg atggccatgg tgggtgtacc tatacaaacg ggcccggagg 120
 ccaatttagc gtcaattggg ctaactccgg aaacttcgta ggtgggaaaag gtcggcaacc 180
 5 cgggaccaaa aataagggtga tcaacttttc tggatcttat aatccgaatg ggaattcata 240
 cttaagcgtc tatgggtggg ctgaaaaccc actgattgaa tattacattg tcgaaaattc 300
 cggtaacctac aatccgagta ccggcgccac aaaattaggc gaagtcacta gtgatggatc 360
 cgtatatgat atctaccgta cccaacgctg taatcagcca tcgatcattg gaaccgccac 420
 cttttatcag tactggagtg cttagcgtaa tcatcgagc cccgggtcgg ttaatactgc 480
 10 gaatcacttc aatgcacggg cacagcaagg gttaacccta ggtacaatgg attatcaaat 540
 cgtagcggcg gaaggctact tctcgagtgg ttccgctagt attacagtga gctaaa 596

<210> 19
 15 <211> 40
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:Trx-110C Synthetic Sequence
 20 <400> 19
 atatacggat ccatcacaag lgactcgcc taatttgg 40
 <210> 20
 <211> 68
 <212> DNA
 25 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:Tx-110C-2
 <400> 20

30 ggcgcacaaa attaggcgaa gtcacttggt atggatccgt atatgatata taccgtaccc 60
 aacgcgtt 68

<210> 21
 35 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:Tx-103b
 40 <400> 21
 aatcagccat cgtatcattg aaccgccacc ttatcagt ac 42
 <210> 22
 <211> 64
 <212> DNA
 45 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:XyTv-109
 Synthetic sequence
 <400> 22
 50 ggtggcgggt ccaatgatcg atggctgatt aacgcgttgg gtacggtaga tacc 54
 <210> 23
 <211> 48
 <212> DNA
 <213> Artificial Sequence
 55 <220>
 <223> Description of Artificial Sequence:Tx-108b
 <400> 23
 cgaaccggag ctccgatgat tacgtctaac atccagtagc tgataaaa 48

EP 1 131 447 B1

<210> 24
<211> 52
<212> DNA
<213> Artificial Sequence
5 <220>
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Synthetic sequence
<400> 24
ctagggttaa ccttgtgat gccaggcat taaagtgga tgcagtata ac 52
10 <210> 25
<211> 84
<212> DNA
<213> Artificial Sequence
<220>
15 <223> Description of Artificial Sequence:Tx-154C-2
<400> 25

tggagtgtca gacgtaatca tcggagctcc ggttcgggta atactgcatg ccactttaac 60
20 gcctgggcac agcaaggggc aacc 84

<210> 26
<211> 34
<212> DNA
25 <213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-162H-3
<400> 26
ccactcaat gcatgggca agcacgggtt aacc 34
30 <210> 27
<211> 42
<212> DNA
<213> Artificial Sequence
<220>
35 <223> Description of Artificial Sequence:TrX-162H-4
<400> 27
ctagggttaa ccgtgctgt gccatgcat tgaagtgga tg 42
<210> 28
<211> 58
40 <212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-101
<400> 28
45 tcgacaatt cggtacctac aatccagca ccggcgccac aaaattaggc gaagtcac 58
<210> 29
<211> 52
<212> DNA
<213> Artificial Sequence
<220>
50 <223> Description of Artificial Sequence :XyTv-102
<400> 29
tagtgatgga tccgtatag atatctaccg tcccaacgc gttaatcagc ca 52
<210> 30
55 <211> 60
<212> DNA
<213> Artificial Sequence
<220>

EP 1 131 447 B1

<223> Description of Artificial Sequence:TrX-103
<400> 30
tcgatcatg gaaccgccac cttttatcag tactggagtg ttagacgtaa lcatcggagc 60
<210> 31
<211> 69
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-104
10 <400> 31

tccgggtcgg ttaatactgc gaatcacttt aatgcattggg cacagcaagg gttaacccta 60
ggcacatg 69
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<210> 32
<211> 67
<212> DNA
<213> Artificial Sequence
20 <220>
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<400> 32

gattatcaaa tcgtacgggt ggaaggctac ttctcagtg gtcccgctag tattacagtg 60
agctaaa 67
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<210> 33
<211> 53
30 <212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence:XyTv-106 synthetic sequence
<400> 33
35 gatcittago tcactgaat actagcggaa ccactcgaga agtagcctc cac 53
<210> 34
<211> 66
<212> DNA
<213> Artificial Sequence
40 <220>
<223> Description of Artificial Sequence:XyTv-107
<400> 34

cgctacgatt tgataatcca ttgcacctag ggctaaccct tgctgtgccc atgcattaaa 60
gtgatt 66
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<210> 35
<211> 60
50 <212> DNA
<213> Artificial Sequence.
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<400> 35
55 cgcagtatta accgaaccgg agctccgatg attacgcta acactccagt actgataaaa 60
<210> 36
<211> 73
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EP 1 131 447 B1

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:XyTv-110

<400> 36

5 atatacggat ccatcactag tgacttcgcc taattttgtg gcgcgggtac tggattgta 60
ggtaaccgaaa ctg 73

10 <210> 37
<211> 76
<212> DNA
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<223> Description of Artificial Sequence:TrX-1

<400> 37

15 ctagctaagg aggctgcaga tgcaaacat acaaccagga accggttaca acaacggtta 60
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<210> 38

<211> 78

<212> DNA

25 <213> Artificial Sequence

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<223> Description of Artificial Sequence:XyTv-2

<400> 38

30 aacgatggcc atggtgggtg taccratata aacggggcccg gaggccaatt tagcgtcaat 60
tggcttaact ccggaaac 78

35 <210> 39
<211> 78
<212> DNA
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<223> Description of Artificial Sequence:TrX-3

<400> 39

40 ttctgtaggcg gaaaagggtg gcaaccggg accaanaata aggtgatcaa ctctctctgga 60
tcttataatc cgaatggg 78

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<210> 40

<211> 74

<212> DNA

50 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:XyTv-4

<400> 40

55 aattcact taagcgtcta cggctgggtc agaaaccac tgattgaata ttacattgtc 60
gaaaatttcg gtac 74

EP 1 131 447 B1

<210> 41
<211> 85
<212> DNA
<213> Artificial Sequence
5 <220>
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gcaaaattttc gacaaatgtaa tattcaatca gtgggtttct agaccagcca tagacgetta 60
10 agtatgaatt cccattcgga ttata 85

<210> 42
<211> 78
15 <212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence:Trx-6Synthetic sequence
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agatccagag aagttgatca ccttatcttc ggtcccgggt tgccaacctt tccacctac 60
gaagtttccg gagttaga 78

25 <210> 43
<211> 84
<212> DNA
<213> Artificial Sequence
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30 <223> Description of Artificial Sequence:XyTv-7
Synthetic sequence
<400> 43
35 ccaattgacg ctaaattggc ctccggggccc gtttgatag gtaacaccac catggccatc 60
gttccaatag ctgtaaaagt aacc 84

40 <210> 44
<211> 51
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence:TrX-8 synthetic
45 sequence
<400> 44
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<210> 45
<211> 40
50 <212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence:Tx-108C
synthetic sequence
55 <400> 45
atatacggat ccatcactcg tgcattcgcc taatttttg 40
<210> 48
<211> 68

EP 1 131 447 B1

<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-108C-2
5 <400> 48
gcgccacaaa attagggcga tgcactagtg atggatccgt atatgatatt taccgtaccc 60
aacgcgtt 68

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<210> 47
<211> 52
<212> DNA
<213> Artificial Sequence
<220>
15 <223> Description of Artificial Sequence:Tx-158C-162H
synthetic sequence
<400> 47
ctagggttaa cccgtgtgat gccagcaat taaagtatt tgcagtatta ac 52
20 <210> 48
<211> 84
<212> DNA
<213> Artificial Sequence
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25 <223> Description of Artificial Sequence:TX-158C-162H-2
<400> 48
tggagtgtta gacgtaatca tcggagctcc ggttcgggta atactgcaaa tcaatttaatt 60
tgctggggcac agcacgggtt aacc 84

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<210> 49
<211> 40
<212> DNA
35 <213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-108c-110c
synthetic sequence
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40 atatacggat ccatcacaag tgcattcgcc taattttgtg 40
<210> 50
<211> 68
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence:Tx-108C-110C-2
synthetic sequence
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50 gcgccacaaa attagggcga tgcactcgtg atggatccgt atatgatatt taccgtaccc 60
aacgcgtt 68

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<210> 51
<211> 52
<212> DNA
<213> Artificial Sequence
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EP 1 131 447 B1

<223> Description of Artificial
Sequence:Tx-154C-155C-152H synthetic sequence

<400> 51

ctagggttaa cccgtgtgat gccagcaat taeagtggca tgcagatta ac 52

<210> 52

<211> 84

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial

Sequence:Tx-154C-158C-162H-2

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tggagtgtta gacgtaatca tccgagctcc ggttcggcta atactgcatg ccactttaac 60
tgctgggcac agcacgggtt aacc 84

<210> 53

<211> 190

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TrX amino acid
sequence

<400> 53.

Gln Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
1 5 10 15

Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
20 25 30

Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
35 40 45

Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly

EP 1 131 447 B1

50 55 60

5 Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65 70 75 80

Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
85 90 95

10 Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
100 105 110

15 Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
115 120 125

Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
130 135 140

20 Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145 150 155 160

Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
165 170 175

25 Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185 190

30 <210> 54
<211> 198
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-DS1
cassette
35 <400> 54

40 gcgccacaaa attaggcgaa gtcacttctg atggatccgt atatgatatt taccgtaccc 60
aacgcgttaa tcagccatcg atcattggaa ccgccacatt ttatcagtag tggagtgtta 120
gacgtaatca tcggagctcc ggctcgggta atactgcatg ccactttaat gcttggggcac 180
agcaagggtt aaccctag 198

45 <210> 55
<211> 67
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial sequence:TrX-DS1
cassette aa
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EP 1 131 447 B1

<400> 55
 Gly Ala Thr Lys Leu Gly Glu Val Thr Cys Asp Gly Ser Val Tyr Asp
 1 5 10 15
 5 Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Thr Ala
 20 25 30
 10 Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg Ser Ser Gly
 35 40 45
 Ser Val Asn Thr Ala Cys His Phe Asn Ala Trp Ala Gln Gln Gly Leu
 50 55 60
 15 Thr Leu Gly
 65

<210> 56
 <211> 15
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:TrX-162H-DS1
 25 cassette aa
 <400> 56

Ala Cys His Phe Asn Ala Trp Ala Gln His Gly Leu Thr Leu Gly
 1 5 10 15
 30

<210> 57
 <211> 198
 <212> DNA
 35 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:TrX-162H-DS2
 cassette
 <400> 57

40 ggcgcacaaa attaggcgaa tgcactagtg atggatccgt atatgatacc taccgtaccc 60
 aacgcgttaa ccagccatcg atcattggaa ccgccaccc ttatcagtag cggagtgtta 120
 gacgtaatca tcggagctcc ggttcgggta atactgc aaa tcactttaat tgctgggcac 180
 agcaacgggtt aaccttag
 45

<210> 58
 <211> 67
 <212> PRT
 50 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:TrX-162H-DS2
 cassette aa
 <400> 58

59

EP 1 131 447 B1

Gly Ala Thr Lys Leu Gly Glu Cys Thr Ser Asp Ser Ser Val Tyr Asp
 1 5 10 15
 5 Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Thr Ala
 20 25 30
 Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg Ser Ser Gly
 35 40 45
 10 Ser Val Asn Thr Ala Asn His Phe Asn Cys Trp Ala Gln His Gly Leu
 50 55 60
 Thr Leu Gly
 65
 15
 <210> 59
 <211> 198
 <212> DNA
 20 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:TrX-162H-DS4
 cassette
 <400> 59
 25
 ggcgcacaaa attaggcgaa tgcacttggtg atggatccgt atatgacatc taccgtaccc 60
 aacgcgttaa tcagccatcg atcattggaa ccgccacctt ttatcagtac tggagtgtta 120
 gacgtaatca tcggaetccc ggttcggtta atactgcatg ccactttaat tgcctggcac 180
 30 agcacgggtt aaccctag 198

35 <210> 60
 <211> 67
 <212> PRT
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence:TrX-162H-DS4
 cassette aa
 40 <400> 60

Gly Ala Thr Lys Leu Gly Glu Cys Thr Cys Asp Gly Ser Val Tyr Asp
 1 5 10 15
 45 Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Thr Ala
 20 25 30
 50

65

EP 1 131 447 B1

Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg Ser Ser Gly
 35 40 45

Ser Val Asn Thr Ala Cys His Phe Asn Cys Trp Ala Gln His Gly Leu
 50 55 60

Thr Leu Gly
 65

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TrX-162H-DS1

cassette

<400> 61

catgccactt caatgcatgg gcacagcacg ggtaacact ag 42

Claims

1. An isolated Family 11 xylanase comprising at least one intramolecular disulphide bond, and a basic amino acid at position 162 (*Trichoderma reesei* xylanase II numbering) or its equivalent, said position determined from sequence alignment of said isolated xylanase with said *Trichoderma reesei* xylanase II amino acid sequence defined in SEQ ID NO:16, said isolated xylanase exhibiting at least 40% of optimal activity, when compared to wild-type xylanase, from pH 3.5 to pH 6.0, and from 40 to 60°C, and at least 30% of optimal activity after a pre-incubation step for 30 minutes at 70°C, 80°C or 90°C in the presence of 40% glycerol; a pre-incubation step for 30 or 60 minutes at 62.5°C in the absence of a stabilizer or a pre-incubation step of 30 minutes at 64°C or 68°C in the absence of a stabilizer.
2. The isolated xylanase of claim 1, wherein said basic amino acid is selected from the group consisting of lysine, arginine and histidine.
3. The isolated xylanase of claim 2, wherein said basic amino acid is histidine.
4. The isolated xylanase of claim 1 comprising two disulfide bridges.
5. The isolated xylanase of claim 1 selected from the group consisting of TrX-162H-DS1, TrX-162H-DS2, TrX-162H-DS4, and TrX-DS8.
6. The isolated xylanase of claim 5, wherein said xylanase is TrX-162H-DS1.
7. The isolated xylanase of claim 5, wherein said xylanase is TrX-162H-DS2.
8. The isolated xylanase of claim 5, wherein said xylanase is TrX-162H-DS4.
9. The isolated xylanase of claim 5, wherein said xylanase is TrX-DS8.
10. A method of obtaining Family 11 xylanase comprising:
 - i) selecting an organism that expresses xylanase activity, and obtaining said xylanase from said organism;
 - ii) determining whether said xylanase exhibits at least 40% of optimal activity, when compared to wild-type xylanase, from pH 3.5 to pH 6.0, and from 40 to 60°C; and
 - iii) determining whether said xylanase is a Family 11 xylanase and exhibits at least 30% of optimal activity after

EP 1 131 447 B1

- a pre-incubation step for 30 minutes at 70°C, 80°C or 90°C in the presence of 40% glycerol;
 a pre-incubation step for 30 or 60 minutes at 62.5°C in the absence of a stabilizer; or
 a pre-incubation step of 30 minutes at 64°C or 68°C in the absence of a stabilizer;
 iv) determining whether said xylanase has a basic amino acid at position 162 (*Trichoderma reesei* xylanase II numbering), said position determined from sequence alignment of said isolated xylanase with said *Trichoderma reesei* xylanase II amino acid sequence defined in SEQ ID NO: 16, and an intra-molecular disulfide bond; and
 v) retaining said xylanase that expresses these properties.
11. The method of claim 10, wherein step i) includes partially purifying said xylanase.
12. A method of preparing animal feed comprising applying the isolated xylanase of claim 1 onto said animal feed to produce a xylanase-animal feed combination, and heat sterilizing said xylanase-animal feed combination.
13. The method of claim 12, wherein said animal feed is a poultry or swine feed.
14. A method of preparing animal feed comprising, applying the xylanase obtained from step v) of claim 10 onto said animal feed to produce a xylanase-animal feed combination, and heat sterilizing said xylanase-animal feed combination.
15. The method of claim 14, wherein said animal feed is a poultry or swine feed.
16. The isolated xylanase of claim 1, wherein the xylanase is recombinant.
17. The isolated xylanase of claim 1 comprising one disulfide bridge.
18. The isolated xylanase of claim 1, said xylanase obtained from an organism selected from the group consisting of *Aspergillus niger*, *Aspergillus kawachii*, *Aspergillus tubingensis*, *Bacillus circulans*, *Bacillus pumilus*, *Bacillus subtilis*, *Cellulomonas fimi*, *Chaetia* spp., *Clostridium acetobutylicum*, *Clostridium stercoarum*, *Fibrobacter succinogenes*, *Neosartillasterix patriciarum*, *Nocardopsis dassonvillei*, *Ruminococcus flavefaciens*, *Schizophyllum commune*, *Streptomyces lividans*, *Streptomyces* sp. No. 36a, *Streptomyces thermoviolaceus*, *Thermomonospora fusca*, *Trichoderma harzianum*, *Trichoderma reesei*, and *Trichoderma viride*.
19. An isolated Family 11 xylanase characterized in comprising at least one intramolecular disulfide bond, and a basic amino acid at position 162 (*Trichoderma reesei* xylanase II numbering) or its equivalent, said position determined from sequence alignment of said isolated xylanase with said *Trichoderma reesei* xylanase II amino acid sequence defined in SEQ ID NO:16, said xylanase exhibiting at least 30% of optimal activity, when compared to wild-type xylanase, after
 a pre-incubation step for 30 minutes at 70°C, 80°C or 90°C in the presence of 40% glycerol;
 a pre-incubation step for 30 or 60 minutes at 62.5°C in the absence of a stabilizer, or
 a pre-incubation step of 30 minutes at 64°C or 68°C in the absence of a stabilizer.

Patentansprüche

1. Isolierte Xylanase der Familie 11, umfassend mindestens eine intramolekulare Disulfid-Bindung und eine basische Aminosäure in Position 162 (*Trichoderma reesei* Xylanase II Nummerierung) oder deren Äquivalent, wobei diese Position durch Sequenzvergleich der genannten isolierten Xylanase mit der Aminosäuresequenz der genannten *Trichoderma reesei* Xylanase II, wie sie in SEQ ID NO:16 definiert ist, festgelegt wurde, wobei die genannte isolierte Xylanase, im Vergleich mit Xylanase vom Wildtyp, mindestens 40% der optimalen Aktivität im Bereich von pH 3,5 bis 6,0 und von 40 bis 60°C zeigt, und nach
 einem 30 minütigen Vorinkubations-Schritt bei 70°C, 80°C oder 90°C in der Gegenwart von 40% Glycerin,
 einem 30- oder 60 minütigen Vorinkubations-Schritt bei 62,5°C in Abwesenheit eines Stabilisators oder
 einem 30-minütigen Vorinkubations-Schritt bei 64°C oder 68°C in Abwesenheit eines Stabilisators
 mindestens 30% der optimalen Aktivität zeigt.
2. Isolierte Xylanase gemäß Anspruch 1, worin die genannte basische Aminosäure ausgewählt ist aus der Gruppe, die aus Lysin, Arginin und Histidin besteht.

EP 1 131 447 B1

3. Isolierte Xylanase gemäß Anspruch 2, worin die genannte basische Aminosäure Histidin ist.
4. Isolierte Xylanase gemäß Anspruch 1, umfassen zwei Disulfid-Brücken.
5. Isolierte Xylanase gemäß Anspruch 1, ausgewählt aus der Gruppe, die aus TrX-162H-DS1, TrX-162H-DS2, TrX-162H-DS4 und TrX-DS8 besteht.
6. Isolierte Xylanase gemäß Anspruch 5, worin die Xylanase TrX-162H-DS1 ist.
7. Isolierte Xylanase gemäß Anspruch 5, worin die Xylanase TrX-162H-DS2 ist.
8. Isolierte Xylanase gemäß Anspruch 5, worin die Xylanase TrX-162H-DS4 ist.
9. Isolierte Xylanase gemäß Anspruch 5, worin die Xylanase TrX-DS8 ist.
10. Verfahren zum Gewinnen einer Xylanase der Familie 11, umfassen:
 - i) Auswählen eines Organismus', der Xylanase-Aktivität exprimiert, und Gewinnen der Xylanase aus diesem Organismus;
 - ii) Feststellen, ob diese Xylanase, im Vergleich mit Xylanase vom Wildtyp, mindestens 40% der optimalen Aktivität im Bereich von pH 3,5 bis pH 6,0 und von 40 bis 60°C zeigt;
 - iii) Feststellen, ob die genannte Xylanase eine Xylanase der Familie 11 ist und nach einem 30-minütigen Vorinkubations-Schritt bei 70°C, 80°C oder 90°C in der Gegenwart von 40% Glycerin, einem 30- oder 60-minütigen Vorinkubations-Schritt bei 62,5°C in Abwesenheit eines Stabilisators oder einem 30-minütigen Vorinkubations-Schritt bei 64°C oder 68°C in Abwesenheit eines Stabilisators mindestens 30% der optimalen Aktivität zeigt;
 - iv) Feststellen, ob die genannte Xylanase eine basische Aminosäure in Position 162 (*Trichoderma reesei* Xylanase 11 Numerierung), wobei diese Position durch einen Sequenzvergleich der genannten isolierten Xylanase mit der Aminosäuresequenz der genannten *Trichoderma reesei* Xylanase II, wie sie in SEQ ID NO:16 definiert ist, festgestellt wird, und eine intramolekulare Disulfid-Bindung besitzt, und
 - v) Gewinnen oder Zurückbehalten der Xylanase, die diese Eigenschaften zeigt.
11. Verfahren nach Anspruch 10, worin Schritt i) das teilweisen Reinigen der Xylanase umfasst.
12. Verfahren zum Herstellen von Tierfutter, umfassend das Aufbringen der isolierten Xylanase gemäß Anspruch 1 auf das Tierfutter, um eine Xylanase-Tierfutter-Kombination zu erzeugen, und Hitzesterilisieren der genannten Xylanase-Tierfutter-Kombination.
13. Verfahren gemäß Anspruch 12, worin das Tierfutter ein Geflügel- oder Schweinefutter ist.
14. Verfahren zum Herstellen von Tierfutter, umfassend das Aufbringen der aus Schritt v) des Anspruchs 10 erhaltenen Xylanase auf das genannte Tierfutter, um eine Xylanase-Tierfutter-Kombination zu erzeugen, und Hitzesterilisieren der genannten Xylanase-Tierfutter-Kombination.
15. Verfahren nach Anspruch 14, worin das Tierfutter ein Geflügel- oder Schweinefutter ist.
16. Isolierte Xylanase gemäß Anspruch 1, worin die Xylanase rekombinant ist.
17. Isolierte Xylanase gemäß Anspruch 1, umfassend eine (einzige) Disulfid-Brücke.
18. Isolierte Xylanase gemäß Anspruch 1, worin die Xylanase aus einem Organismus gewonnen wurde, der ausgewählt ist aus der aus *Aspergillus niger*, *Aspergillus kawachii*, *Aspergillus tubigenensis*, *Bacillus circulans*, *Bacillus pumilus*, *Bacillus subtilis*, *Cellulomonas fimi*, *Chaetia* spp., *Clostridium acetobutylicum*, *Clostridium stercoararium*, *Fibrobacter succinogenes*, *Neocallimastix patriciarum*, *Nocardiopsis dassonvillei*, *Ruminococcus flavefaciens*, *Schizothraustes communis*, *Streptomyces lividans*, *Streptomyces* sp. Nr. 36a, *Streptomyces thermoviolaceus*, *Thermomonospora fusca*, *Trichoderma harzianum*, *Trichoderma reesei* und *Trichoderma viride* umfassenden Gruppe.
19. Isolierte Xylanase der Familie 11, dadurch gekennzeichnet, dass sie mindestens eine intramolekulare Disulfid-

EP 1 131 447 B1

Brücke und eine basische Aminosäure in Position 162 (*Trichoderma reesei* Xylanase 11 Numerierung) oder deren Äquivalent umfasst, wobei diese Position durch Sequenzvergleich der genannten isolierten Xylanase mit der Aminosäuresequenz der genannten *Trichoderma reesei* Xylanase II, wie sie in SEQ ID NO:16 definiert ist, festgelegt wurde, wobei die genannte Xylanase, im Vergleich mit Xylanase vom Wildtyp, nach einem 30 minütigen Vorinkubations-Schritt bei 70°C, 80°C oder 90°C in der Gegenwart von 40% Glycerin, einem 30- oder 60 minütigen Vorinkubations-Schritt bei 62,5°C in Abwesenheit eines Stabilisators oder einem 30-minütigen Vorinkubations-Schritt bei 64°C oder 68°C in Abwesenheit eines Stabilisators mindestens 30% der optimalen Aktivität zeigt.

Revendications

1. Xylanase isolée de la famille 11 comprenant au moins un pont disulfure intramoléculaire, et un acide aminé basique à la position 162 (numérotation de la xylanase II de *Trichoderma reesei*) ou son équivalent, ladite position étant déterminée à partir de l'alignement de séquence de ladite xylanase isolée avec ladite séquence d'acides aminés de la xylanase II de *Trichoderma reesei* définie dans SEQ ID N° : 16, ladite xylanase isolée présentant au moins 40 % d'activité optimale lorsqu'elle est comparée à la xylanase de type sauvage de pH 3,5 à pH 6,0, et de 40 à 60°C, et au moins 30 % d'activité optimale après une étape de pré-incubation de 30 minutes à 70°C, 80°C ou 90°C en présence de 40 % de glycérol ;
 une étape de pré-incubation de 30 ou 60 minutes à 62,5°C en l'absence d'un stabilisateur ; ou
 une étape de pré-incubation de 30 minutes à 64°C ou 68°C en l'absence d'un stabilisateur.
2. Xylanase isolée selon la revendication 1, dans laquelle ledit acide aminé basique est choisi dans le groupe constitué par la lysine, l'arginine et l'histidine.
3. Xylanase isolée selon la revendication 2, dans laquelle ledit acide aminé basique est l'histidine.
4. Xylanase isolée selon la revendication 1, comprenant deux ponts disulfure.
5. Xylanase isolée selon la revendication 1, choisie dans le groupe constitué par TrX-162H-DS1, TrX-162H-DS2, TrX-162H-DS4, et TrX-DS8.
6. Xylanase isolée selon la revendication 5, dans laquelle ladite xylanase est TrX-162H-DS1.
7. Xylanase isolée selon la revendication 5, dans laquelle ladite xylanase est TrX-162H-DS2.
8. Xylanase isolée selon la revendication 5, dans laquelle ladite xylanase est TrX-162H-DS4.
9. Xylanase isolée selon la revendication 5, dans laquelle ladite xylanase est TrX-DS8.
10. Procédé d'obtention d'une xylanase de la famille 11, comprenant :
 - i) la sélection d'un organisme qui exprime l'activité xylanase, et l'obtention de ladite xylanase dudit organisme ;
 - ii) la détermination du fait que la xylanase présente ou non au moins 40 % d'activité optimale lorsqu'elle est comparée à la xylanase de type sauvage de pH 3,5 à pH 6,0, et de 40 à 60°C ; et
 - iii) la détermination du fait que ladite xylanase est une xylanase de la famille 11 et présente au moins 30 % d'activité optimale après
 une étape de pré-incubation de 30 minutes à 70°C, 80°C ou 90°C en présence de 40 % de glycérol ;
 une étape de pré-incubation de 30 ou 60 minutes à 62,5°C en l'absence d'un stabilisateur ; ou
 une étape de pré-incubation de 30 minutes à 64°C ou 68°C en l'absence d'un stabilisateur ;
 - iv) la détermination du fait que ladite xylanase a ou non un acide aminé basique à la position 162 (numérotation de la xylanase II de *Trichoderma reesei*), ladite position étant déterminée à partir de l'alignement de séquence de ladite xylanase isolée avec ladite séquence d'acides aminés de la xylanase II de *Trichoderma reesei* définie dans SEQ ID N° : 16, et un pont disulfure intramoléculaire ; et
 - v) la conservation de ladite xylanase qui exprime ces propriétés.
11. Procédé selon la revendication 10, dans lequel l'étape i) comprend la purification partielle de ladite xylanase.

EP 1 131 447 B1

12. Procédé de préparation de nourriture pour animaux comprenant l'application de la xylanase isolée selon la revendication 1 sur ladite nourriture pour animaux pour produire une combinaison de xylanase-nourriture pour animaux, et la stérilisation thermique de ladite combinaison de xylanase-nourriture pour animaux.
13. Procédé selon la revendication 12, dans lequel ladite nourriture pour animaux est de la nourriture pour la volaille ou les porcs.
14. Procédé de préparation de nourriture pour animaux comprenant l'application de la xylanase obtenue dans l'étape v) de la revendication 10 sur ladite nourriture pour animaux pour produire une combinaison xylanase-nourriture pour animaux, et la stérilisation thermique de ladite combinaison de xylanase-nourriture pour animaux.
15. Procédé selon la revendication 14, dans lequel ladite nourriture pour animaux est de la nourriture pour la volaille ou les porcs.
16. Xylanase isolée selon la revendication 1, dans laquelle la xylanase est recombinante.
17. xylanase isolée selon la revendication 1, comprenant un pont disulfure.
18. Xylanase isolée selon la revendication 1, ladite xylanase étant obtenue à partir d'un organisme choisi dans le groupe constitué par *Aspergillus niger*, *Aspergillus kawachii*, *Aspergillus tubingensis*, *Bacillus circulans*, *Bacillus pumilus*, *Bacillus subtilis*, *Cellulomonas fimi*, *Chelonia spp.*, *Clostridium acetobutylicum*, *Clostridium stercorarium*, *Fibrobacter succinogenes*, *Neocallimastix patriciarum*, *Nocardiopsis dassonvillei*, *Ruminococcus flavefaciens*, *Schizophyllum commune*, *Streptomyces lividans*, *Streptomyces sp. No. 36a*, *Streptomyces thermoviolaceus*, *Thermomonospora fusca*, *Trichoderma harzianum*, *Trichoderma reesei*, et *Trichoderma viride*.
19. Xylanase isolée de la famille 11 caractérisée en ce qu'elle comprend au moins un pont disulfure intramoléculaire, et un acide aminé basique à la position 182 (numérotation de la xylanase II de *Trichoderma reesei*) ou son équivalent, ladite position étant déterminée à partir de l'alignement de séquence de ladite xylanase isolée avec ladite séquence d'acides aminés de la xylanase II de *Trichoderma reesei* définie dans SEQ ID N° : 16, ladite xylanase isolée présentant au moins 30 % d'activité optimale lorsqu'elle est comparée à la xylanase de type sauvage après une étape de pré-incubation de 30 minutes à 70°C, 80°C ou 90°C en présence de 40 % de glycérol ; une étape de pré-incubation de 30 ou 60 minutes à 62,5°C en l'absence d'un stabilisateur ; ou une étape de pré-incubation de 30 minutes à 64°C ou 68°C en l'absence d'un stabilisateur.

EP 1 131 447 B1

				S	AFNTQAAP	31
				G		1
Ca	23					
Cs	1					
Bp	1	RTITNNEMGN	HSGYDYELWK DYGNT-SMTL NNGGAFSAGW N--NIGNA			45
Ca	32	KTITSNEIGV	NGGYDYELWK DYGNT-SMTL KNGGAFSCQW S--NIGNA			76
Cs	2	RIIYDNETGT	HGGYDYELWK DYGNT-IMEL NDGGTFSCQW S--NIGNA			46
Rf	1	SAADQOTRGN	VGGYDYEMWN QNGGQASMN PGAGSFTCSW S--NIENF			46
Tr2	1	QTIQPGTGY	NNGYFYSYWN DGHGGVITYN GPGGQFSVWN S--NSGNF			45
Tv	1	QTIQPGTGF	NNGYFYSYWN DGHGGVITYN GPGGQFSVWN S--NSGNF			45
Th	1	QTIQPGTGY	SNGYFYSYWN DGHAGVITYN GGGGSFTVWN S--NSGNF			45
Sc	1	SGTPSSTGT	DGGYYSWWT DGAGDATYON NGGGSYTLTH SG--NNGNL			46
An	1		AGINYVQNYN GNLGDFTY-D ESAGTFSMYN EDGVSSDF			38
AT	1		AGINYVQNYN QNLGDFTY-D ESAGTFSMYN EDGVSSDF			38
Tr1	1		ASINYDQNYO TGG-QVSYN PSNTGFSVWN N--TQDDF			34
Ss	1	ATTIT-NETGY	D-GMYSPWT DGGGSVSMIL NCGGSYSTRN T--NCGNF			45
SlB	1	DTVVITNQEGT	MNGYYSFWT DSQGTVMNM GSGGQYSTSW R--NTGNF			47
SlC	1	ATTITNQGT	D-GMYSPWT DGGGSVSMIL NCGGSYSTQN T--NCGNF			46
Tf	1	AVTSNETGY	HDGYFYSFWT DAPGTVMEL GPGGNYSTSW R--NTGNF			45
Bc	1		ASTDYNQNW T DGGGIVNAV N GSGGNYSVNH S--NTGNF			36
Bs	1		ASTDYNQNW T DGGGIVNAV N GSGGNYSVNH S--NTGNF			36
Bp	46	LFRK-GKKFD	ST-RTHQLG NISINYNASF N-PSGNSYLC VYGHQSP			90
Ca	77	LFRK-GKKFN	DT-QTYKQLG NISVNYNCNY Q-PYGNSYLC VYGHQSSP			121
Cs	47	LFRK-GKKFN	SD-KTYQLG DIVVEYGCDY N-PNGNSYLC VYGHTRNP			91
Rf	47	LARM-GKNYD	SQKQNYKAFG NIVLTYDVEY T-PRGNSYMC VYGHTRNP			92
Tr2	46	VGGK-GWQPG	TKNKV-----INFS-GS YNPNGNSYLS VYGHSRNP			83
Tv	46	VGGK-GWQPG	TKNKV-----INFS-GS YNPNGNSYLS VYGHSRNP			83
Th	46	VGGK-GWQPG	TKNKV-----INFS-GS YNPNGNSYLS VYGHTRSS			84
Sc	47	VGGK-GWNP	AASRS-----ISYS-GT YQPNGNSYLS VYGHVNYN			76
An	39	VVGL-GWTTG	SSNA-----ITYSABY SASGSASYLA VYGHVNYN			77
At	39	VVGLGWTTC	SSNA-----INFGGSP SVN5GTCLLS VYGHSTNP			72
Tr1	35	VVGK-GWTTG	SSAP-----VRYT-GW FNPNGNGYGC LYGHSTNP			82
Ss	46	VAGK-GWANG	GR-RT-----VOYS-GS FNPNGNAYLA LYGHSTNP			84
SlB	48	VAGK-GWANG	GR-RT-----VRYN-GY FNPVNGYTOC LYGHSTNP			82
SlC	47	VAGK-GWSTG	DGN-----VTYS-AS FNPNGNAYLT LYGHTRNP			82
Tf	46	VAGK-GWATG	GR-RT-----INYNAGV WAPNGNGYLT LYGHTRSP			75
Bc	37	VVGK-GWTTG	SPFRT-----INYNAGV WAPNGNGYLT LYGHTRSP			75
Bs	37	VVGK-GWTTG	SPFRT-----INYNAGV WAPNGNGYLT LYGHTRSP			75

FIGURE 1

EP 1 131 447 B1

Bp 91 LAEYIVDSW GTYR-PT--G AYKGSFYADG GTYDIYETTR VNQPSIIG 135
 Ca 122 LVEYVIDSW GSWRPP--GG TSKGTITVDG GIYDIYETTR INQPSIQG 167
 Cs 92 LVEYVIVESW GSWRPP--GA TPKGTITQWMAETIYETTR VNQPSIDG 138
 Rf 93 LMEYIVEGW GDWRPPGNDG EVKQTVSANG NTYDIRKTR VNQPSIDG 140
 Tr2 84 LIEYIVENF GTYN-PTGA TKLGEVTSBG SVYDIYRTOR VNQPSIIG 130
 Tv 84 LIEYIVENF GTYN-PTGA TKLGEVTSBG SVYDIYRTOR VNQPSIIG 130
 Th 84 LIEYIVENF GTYN-PTGA TKLGEVTSBG SVYDIYRTOR VNQPSIIG 130
 Sc 85 LIEYIVESY GSYD-PSSAA SHKGSVTCNG ATYDILSTWR VNPBSIDG 131
 An 77 GAEYIVEDY GDYN-PCSSA TSLGTVYSBG STYQVCTDR INEBSITG 123
 Ac 78 GAEYIVEDY GDYN-PCSSA TSLGTVYSBG STYQVCTDR INEBSITG 124
 Tr1 73 LVEYIMEON HNY--PAQ-G TVKGTVTSBG ATYTIWENTR VNEBSIQG 117
 Ss 83 LVEYIVDNW GSYR-PT--G ETRGTVHSBG GTYDIYKTR VNPBSVEG 127
 SlB 85 LVEYIVDNW GTYR-PT--G EYKGTVTSBG GTYDIYKTR VNPBSVEG 129
 SlC 83 LVEYIVDNW GSYR-PT--G TYKGTVSSBG GTYDIYQTR VNPBSIEG 127
 Tf 83 LVEYVIVESW GTYR-PT--G TYMGTVTIDG GTYDIYKTR VNPBSIEG 127
 Bc 76 LIEYVVDSW GTYR-PT--G TYKGTVKSBG GTYDIYTTTR VNPBSIDG 120
 Bs 76 LIEYVVDSW GTYR-PT--G TYKGTVKSBG GTYDIYTTTR VNPBSIDG 120

Bp 136 -IATEKQYWE VRQTKRTS-- -----GTVS VSAHFRKYES LQMPM-GK 174
 Ca 168 -NTTEKQYWE VRTKRTS-- -----GTIS VSKHPAAHES KQMLP-GK 206
 Cs 139 -TATEQQYWE VRTSKRTS-- -----GTIS VTEHFKQNER MGRM-GK 177
 Rf 141 -TATEPQYWE VEQTSGSAMN QTNMKGITD VSKHFDANSA AGLDMSGT 187
 Tr2 131 -TATEYQYWE VRRNHR-S-S -----GSVN TANHFNAHAQ QGLTL-GT 168
 Tv 131 -TATEYQYWE VRRTHR-S-S -----GSVN TANHFNAHAQ QGLTL-GT 168
 Th 131 -TATEYQYWE VRRNHR-S-S -----GSVN TANHFNAHAQ QGLTL-GT 168
 Sc 132 -TQTLEQFWE VRRNPKAPGG SIS---GTVD VOCHFDANKG LQNNLGSE 175
 An 124 -TSTETQYFE VRESTRTS-- -----GTVT VANHFNFNAH HGFEN-SD 163
 Ac 125 -TSTETQYFE VRESTRTS-- -----GTVT VQNHFN-WAS LGLHLGQM 155
 Tr1 118 -TATENQYIS VRNSPR-T-S -----GTIT TGNHFDANAR AGMNMGNF 168
 Ss 128 -PAAEQYWE VRQSKVT--S -----GTIT TGNHFDANAR AGMPLGNF 168
 SlB 130 TR-TEDQYWE VRQSKR-TG- -----GTIT TGNHFDANAR AGNMNGQF 168
 SlC 128 TK-TEDQYWE VRQSKVTSGS -----GTIT TGNHFDANAR AGMNLGTH 166
 Tf 128 TR-TEDQYWE VRQSKRTS-- -----GTIT TGNHFDANAR AGMNLGTH 166
 Bc 121 DRTTETQYWE VRQSKRPTGS N-----ATIT FSNHVNANKS HGMNLGSN 163
 Bs 121 DRTTETQYWE VRQSKRPTGS N-----ATIT FSNHVNANKS HGMNLGSN 163

FIGURE 1 (CONT'D)

EP 1 131 447 B1

Bp	174	MYETAFTVEG	YQSSGSANVM	TNQLFIGN	201
Ca	207	MHETAFNIEG	YQSSGKADVN	SMSINICK	233
Cs	178	MYEVALTVEG	YQSSGYANVY	KNEIRIGANP....	
Rf	188	LYEVSLNIEG	YRSNGSANVK	SVSV	211
Tr2	169	MDYQIVAVEG	YFSSGSASI-	TVS	190
Tv	169	MDYQIVAVEG	YFSSGSASI-	TVS	190
Th	169	MDYQIVAVEG	YFSSGSASI-	TVS	190
Sc	176	HNYQIVATEG	YQSSGTATI-	TVT	197
An	163	FNYQVMAVEA	WCGAGSASV-	TISS	184
At	164	FNYQVMAVEA	WCGAGSAAV-	TISS	185
Tr1	156	MNYQVVAVEG	WCGSGSASQ-	SVSN	178
Ss	167	RYYMINATEG	YQSSGSSTI-	TVSG	189
SlB	169	SYMINATEG	YQSSGTSSI-	NVGG.....	
SlC	169	RYYMINATEG	YQSSGSSNI-	TVSG	191
Tf	167	D-YMIMATEG	YQSSGSSNVT	LGTS.....	
Bc	164	WAYQVMATEG	YQSSGSSNV-	TVW	185
Bs	164	WAYQVMATEG	YQSSGSSNV-	TVW	185

Bp	<i>Bacillus pumilus</i>
Ca	<i>Clostridium acetobutylicum</i> P262 XynB
Cs	<i>Clostridium stercorarium</i> xynA
Rf	<i>Ruminococcus flavefaciens</i>
Tr2	<i>Trichoderma reesei</i> XYN II
Tv	<i>Trichoderma viride</i>
Th	<i>Trichoderma harzianum</i>
Sc	<i>Schizophyllum commune</i> Xylanase A
An	<i>Aspergillus niger</i> , var. <i>awamori</i>
At	<i>Aspergillus tubigenis</i>
Tr1	<i>Trichoderma reesei</i> XYN I
Ss	<i>Streptomyces</i> sp. 36a
SlB	<i>Streptomyces lividans</i> Xln B
SlC	<i>Streptomyces lividans</i> Xln C
Tf	<i>Thermomonospora fusca</i> TfxA
Bc	<i>Bacillus circulans</i>
Bs	<i>Bacillus subtilis</i>

FIGURE 1 (CONT'D)

EP 1131 447 B1

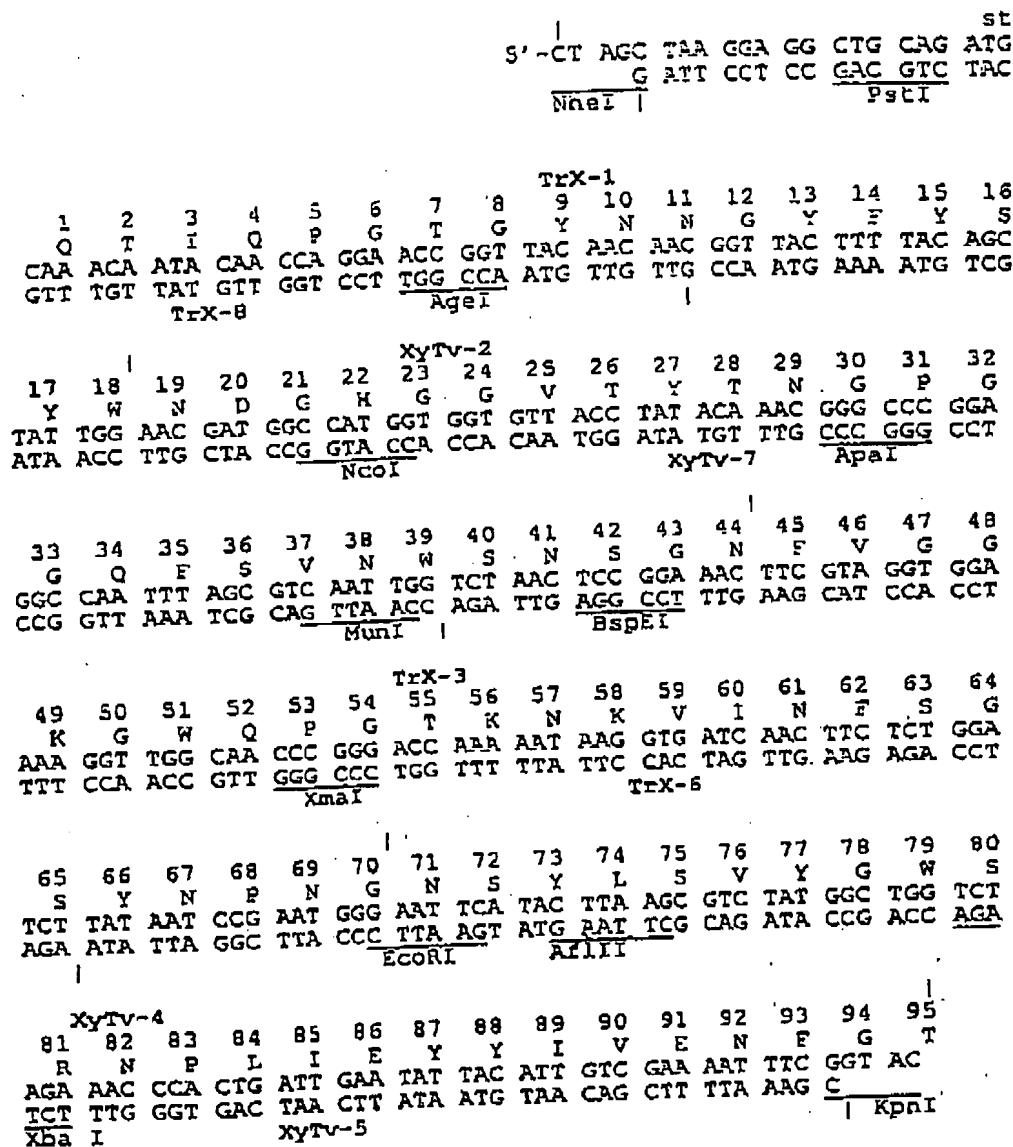


FIG. 2

EP 1 131 447 B1

1
 V D 92 93 94 95 96 97 98 99 100 101 102 103 104 105
 TC GAC AAT TTC GGT ACC TAC AAT CCG AGT ACC GGC GCC ACA AAA TTA
 G TTA AAG CCA TGG ATG TTA GGC TCA TGG CCG CGG TGT TTT AAT
 SalI KpnI XyTV-101 XyTV-110 Kasi/Nari
 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121
 G E V T S D G S V Y D I Y R T Q
 GGC GAA GTC ACT AGT GAT GGA TCC GTA TAT GAT ATC TAC CGT ACC CAA
 CCG CTT CAG TGA TCA CTA CCT AGG CAT ATA CTA TAG ATG GCA TGG GTT
 SpeI BamHI XyTV-102 XyTV-109
 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137
 R V N Q P S I I G T A T F Y Q Y
 CGC GTT AAT CAG CCA TCG ATC ATT GGA ACC GCC ACC TTT TAT CAG TAC
 CCG CAA TTA GTC GGT AGC TAG TAA CCT TGG CCG TGG AAA ATA GTC ATG
 MluI ClaI Trx-103
 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153
 W S V R N H R S S G S V N T A
 TGG AGT GTT AGA CGT AAT CAT CGG AGC TCC GGT TCG GTT AAT ACT GCG
 ACC TCA CAA TCT GCA TTA GTA GCC TCG AGG CCA AGC CAA TTA TGA CGC
 Trx-108 SacI
 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169
 N H F N A W A Q Q G L T L G T M
 AAT CAC TTT AAT GCA TGG GCA CAG CAA GGG TTA ACC CTA GGT ACA ATG
 TTA GTG AAA TTA CGT ACC CGT GTC GTT CCC AAT TGG GAT CCA TGT TAC
 NsiI XyTV-104 XyTV-107 AvrII
 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185
 D Y Q I V A V E G Y F S S G S A
 GAT TAT CAA ATC GTA GCG GTG GAA GGC TAC TTC TCG AGT GGT TCC GCT
 CTA ATA GTT TAG CAT CCG CAC CTT CCG ATG AAG AGC TCA CCA AGG CGA
 XyTV-105 XyTV-106 XhoI
 186 187 188 189 190
 S I T V S
 AGT ATT ACA GTG AGC TAA A
 TCA TAA TGT CAC TCG ATT TCT AG
 BglII

FIG. 2 (CONT'D)

EP 1 131 447 B1

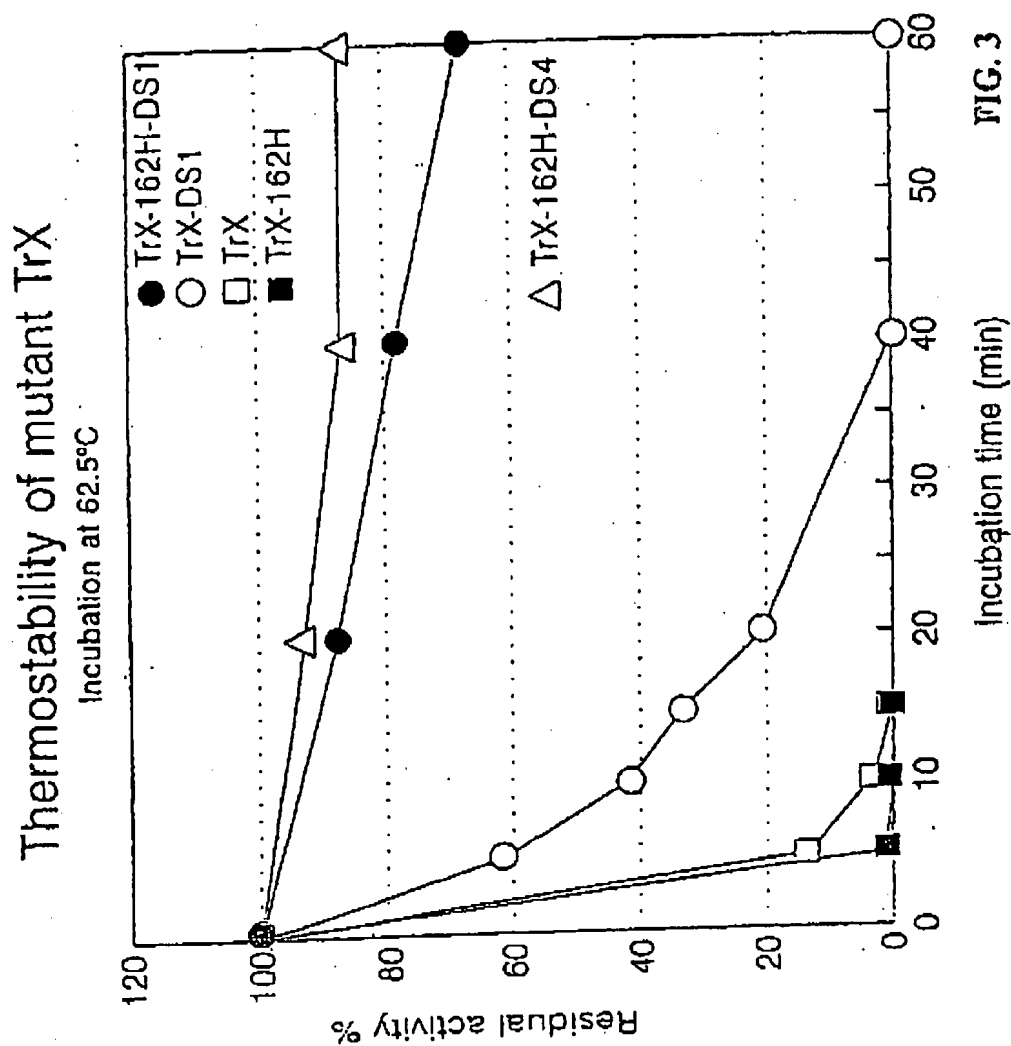


FIG. 3

EP 1 131 447 B1

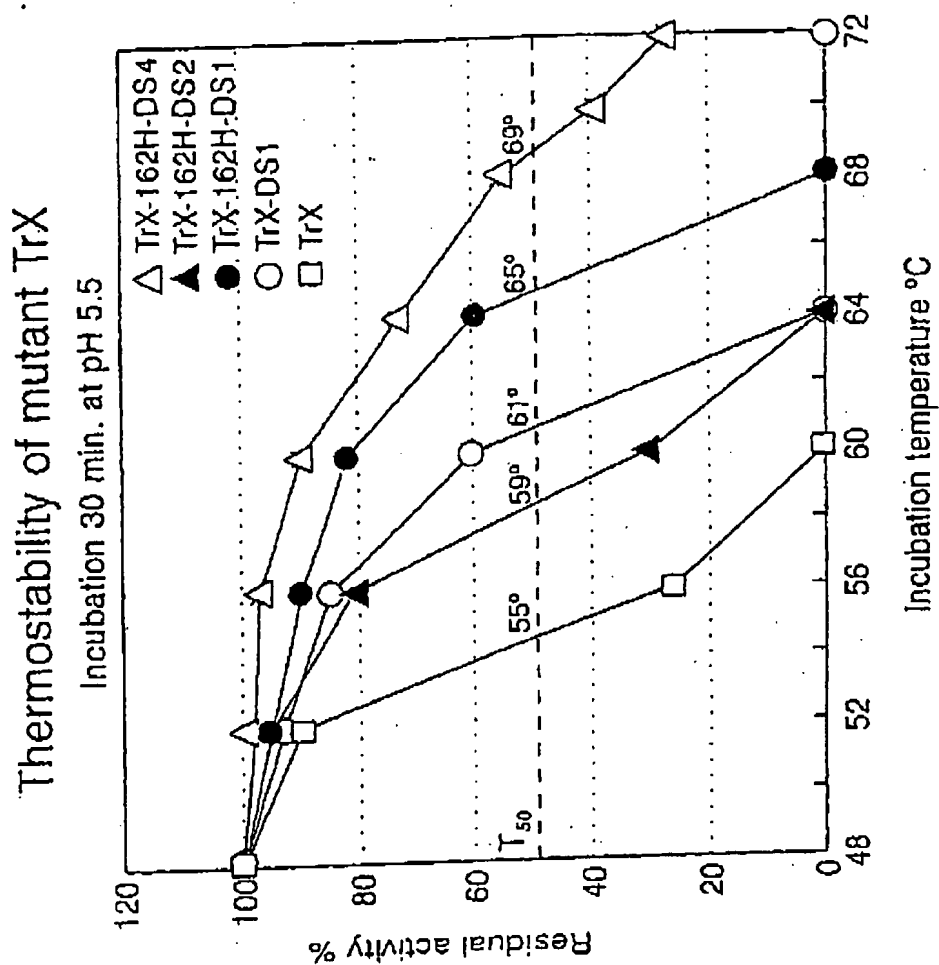
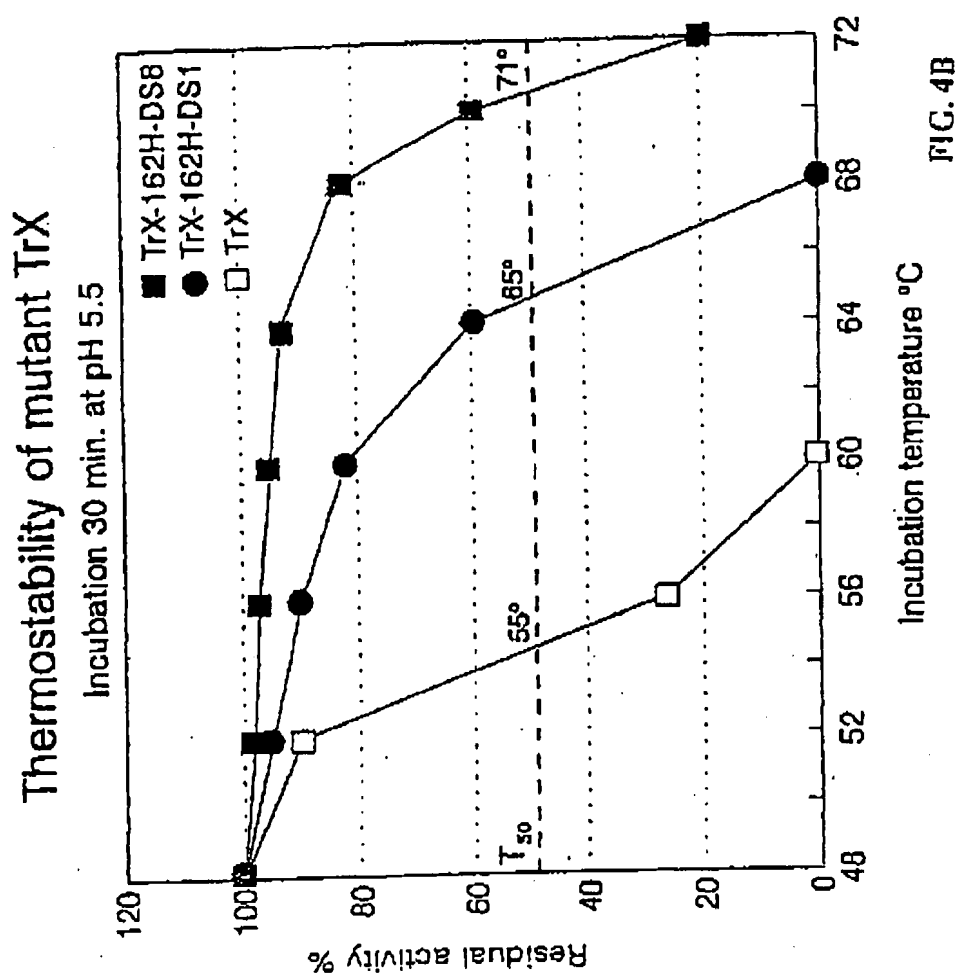


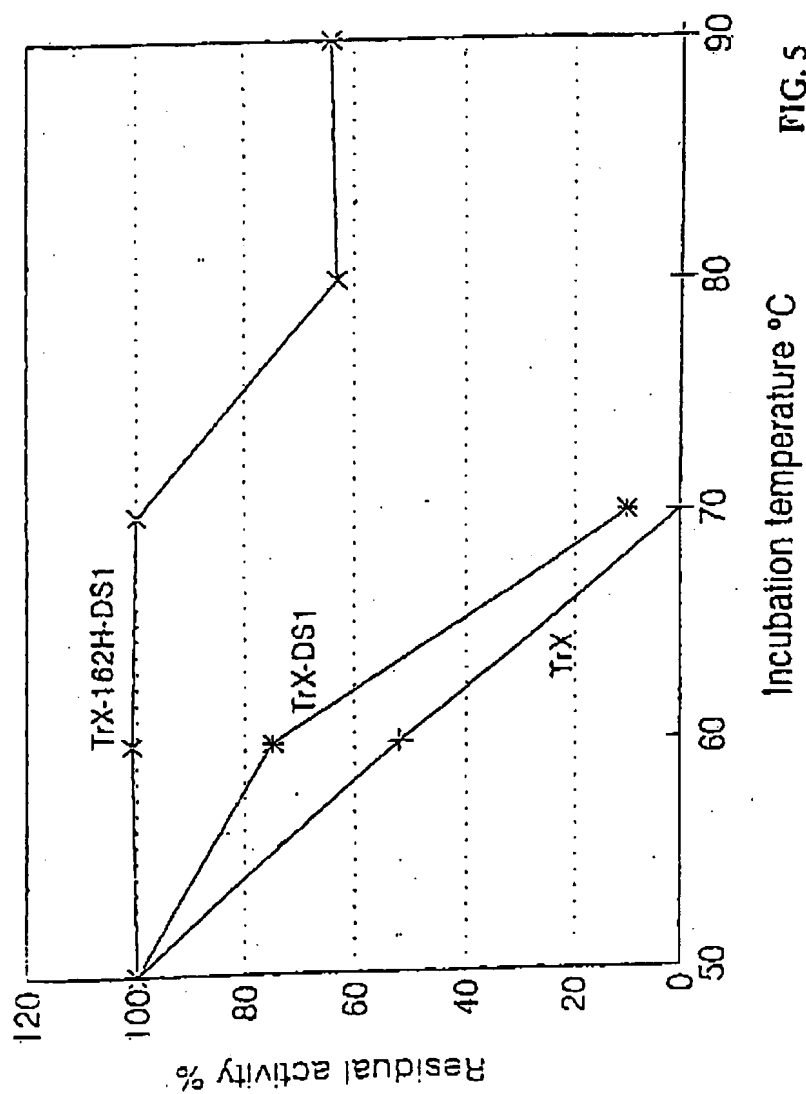
FIG. 4A

EP 1 131 447 B1



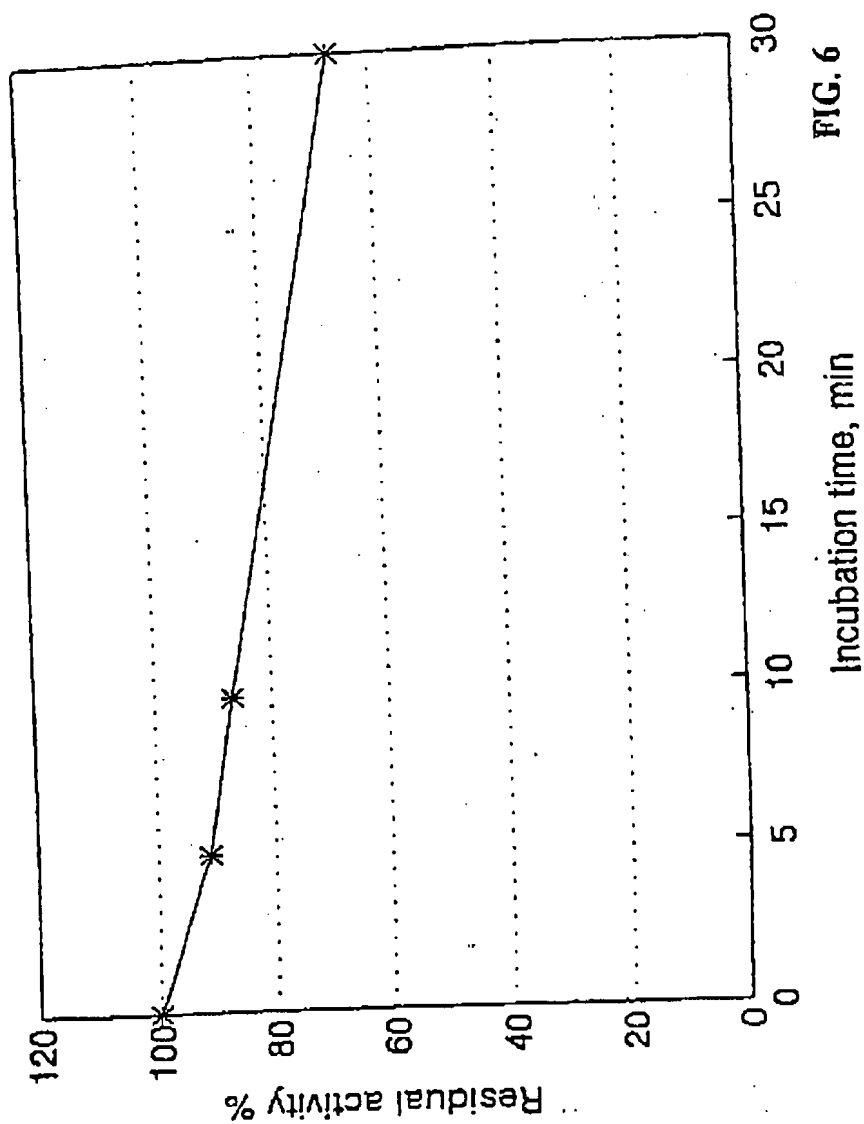
EP 1 131 447 B1

Thermostability of mutant TrX
incubation in 40% glycerol, 30 min



EP 1 131 447 B1

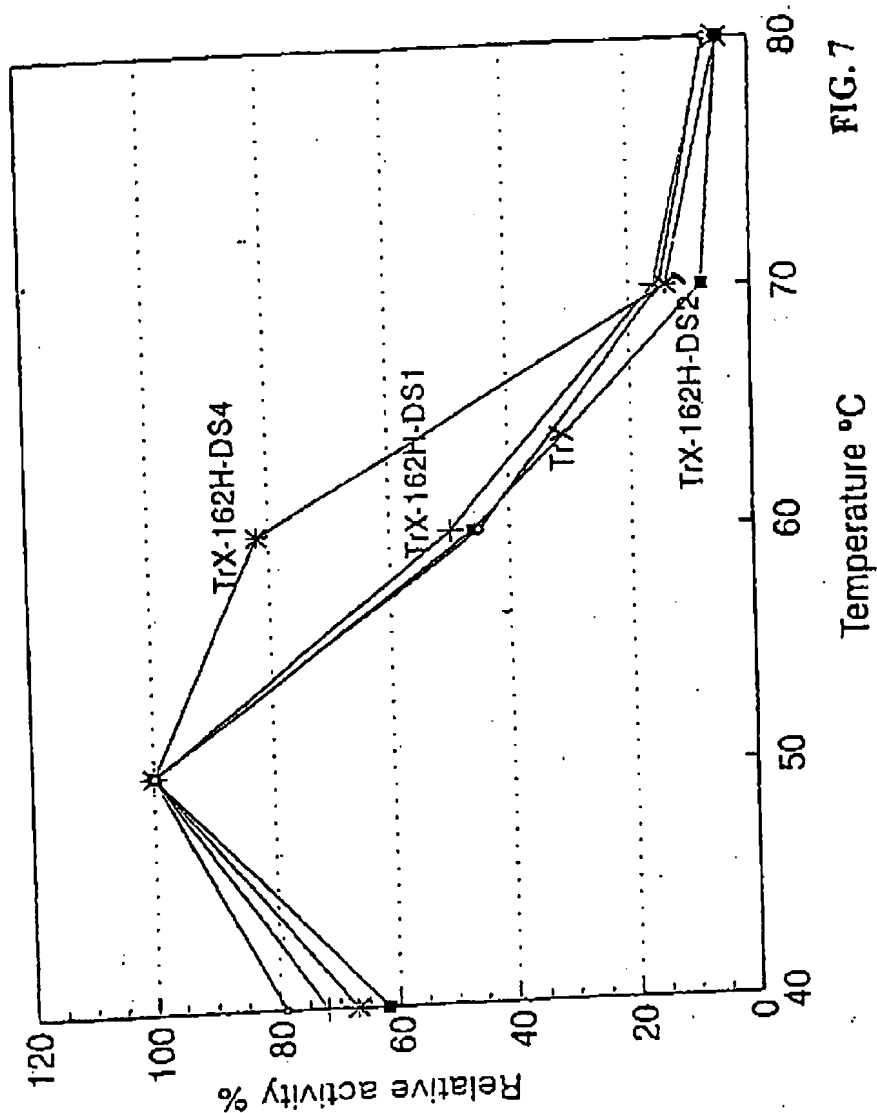
Thermostability of TrX-162H-DS1 at 90°C



EP 1 131 447 B1

Effect of temperature on the hydrolysis of xylan by mutant TrX

pH 4.5, 30 min, 1.5 microgram of each enzyme



EP 1 131 447 B1

